SEQUENCE LISTING

<110> Reed, John C.

<120> Plant Cytoprotective Genes and Methods
of Using Same

<130> P-LJ 4868

<150> US 09/661,014
<151> 2000-09-13

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 617
<212> DNA
<213> Lycopersicon esculentum

<220>
<221> CDS
<222> (103)...(594)

<400> 1
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cgttctctga tgcgtagctg aagaaatatc accggaaagt tcacaggaaa taagtggcgg 60
cggtgcgtgg ctcttgttga ataccaagcg agaggagata ag atg ccg gaa cat    114
                                               Met Pro Glu His
                                               1


cct gct gca gac tca tca gcc acc gac aac acc gtc acc gtc aag cgt    162
Pro Ala Ala Asp Ser Ser Ala Thr Asp Asn Thr Val Thr Val Lys Arg
 5                  10                  15                  20


tat gcc cct ccc aat cag cgg aat cgt tca ctc ggc agg cga aaa tct    210
Tyr Ala Pro Pro Asn Gln Arg Asn Arg Ser Leu Gly Arg Arg Lys Ser
                25                  30                  35


gga gat cga ctt gaa aga gct agc agc tat gct agt gat gga gag aag    258
Gly Asp Arg Leu Glu Arg Ala Ser Ser Tyr Ala Ser Asp Gly Glu Lys
            40                  45                  50


aac caa atg aga gca gct aag tct gta tct gat gct gga gtc aat cga    306
Asn Gln Met Arg Ala Ala Lys Ser Val Ser Asp Ala Gly Val Asn Arg
            55                  60                  65


gta aat gat tat cct cca aca aag tta ata ccg cta caa gga tgt tgt    354
Val Asn Asp Tyr Pro Pro Thr Lys Leu Ile Pro Leu Gln Gly Cys Cys
            70                  75                  80


aca agc gaa gct ttt cag cta cta aat gac cgc tgg gca gct gct ctg    402
```

```
Thr Ser Glu Ala Phe Gln Leu Leu Asn Asp Arg Trp Ala Ala Ala Leu
 85                  90                  95                 100
```

```
aat gct cat aat aat tta tca gaa gat tct cgt gaa agg cct gta atg    450
Asn Ala His Asn Asn Leu Ser Glu Asp Ser Arg Glu Arg Pro Val Met
                105                 110                 115
```

```
tac aca aaa aga tca cct tgg ggg cat cct ttt ctt cca cat caa ttg    498
Tyr Thr Lys Arg Ser Pro Trp Gly His Pro Phe Leu Pro His Gln Leu
                120                 125                 130
```

```
atg tca caa gca gga gct gaa tct tct act ggc cag aag gat ttt cta    546
Met Ser Gln Ala Gly Ala Glu Ser Ser Thr Gly Gln Lys Asp Phe Leu
            135                 140                 145
```

```
agc aaa ctt cag atg gct atg ctc aat aca cat gtc aat ttc gat gcc    594
Ser Lys Leu Gln Met Ala Met Leu Asn Thr His Val Asn Phe Asp Ala
        150                 155                 160
```

```
taaatgctat ccatcaagtg gtc                                          617
```

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<210> 2
<211> 164
<212> PRT
<213> Lycopersicon esculentum

<400> 2
Met Pro Glu His Pro Ala Ala Asp Ser Ser Ala Thr Asp Asn Thr Val
  1               5                  10                  15
Thr Val Lys Arg Tyr Ala Pro Pro Asn Gln Arg Asn Arg Ser Leu Gly
            20                  25                  30
Arg Arg Lys Ser Gly Asp Arg Leu Glu Arg Ala Ser Ser Tyr Ala Ser
        35                  40                  45
Asp Gly Glu Lys Asn Gln Met Arg Ala Ala Lys Ser Val Ser Asp Ala
        50                  55                  60
Gly Val Asn Arg Val Asn Asp Tyr Pro Pro Thr Lys Leu Ile Pro Leu
65                  70                  75                  80
Gln Gly Cys Cys Thr Ser Glu Ala Phe Gln Leu Leu Asn Asp Arg Trp
                85                  90                  95
Ala Ala Ala Leu Asn Ala His Asn Asn Leu Ser Glu Asp Ser Arg Glu
            100                 105                 110
Arg Pro Val Met Tyr Thr Lys Arg Ser Pro Trp Gly His Pro Phe Leu
            115                 120                 125
Pro His Gln Leu Met Ser Gln Ala Gly Ala Glu Ser Ser Thr Gly Gln
            130                 135                 140
Lys Asp Phe Leu Ser Lys Leu Gln Met Ala Met Leu Asn Thr His Val
145                 150                 155                 160
Asn Phe Asp Ala
```

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<210> 3
<211> 1034
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<212> DNA
<213> Lycopersicon esculentum

<220>
<221> CDS
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<223> n = A,T,C or G

<400> 3
gagcaaacat aacattgtct acgttcagat aaatatcctt tgctcatttc agttccaaaa    60
actcgaagaa gaagaagaag agaaca atg gaa ggt ttc aca tcg ttc ttc gac   113
                             Met Glu Gly Phe Thr Ser Phe Phe Asp
                               1               5

tcg caa tct gcc tct cgc aac cgc tgg agt tat gat tct ctc aaa aac   161
Ser Gln Ser Ala Ser Arg Asn Arg Trp Ser Tyr Asp Ser Leu Lys Asn
 10              15                  20                  25

ttc cgc cag atc tca cct ctc gtt caa act cat ctc aag cag gtg tac   209
Phe Arg Gln Ile Ser Pro Leu Val Gln Thr His Leu Lys Gln Val Tyr
                 30                  35                  40

ctt acg cta tgc tgt gct tta gtg gca tcg gct gct ggg gct tac ctt   257
Leu Thr Leu Cys Cys Ala Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu
             45                  50                  55

cac att cta tgg aat atc ggt ggc ctc ctc aca aca atg gct tgc atg   305
His Ile Leu Trp Asn Ile Gly Gly Leu Leu Thr Thr Met Ala Cys Met
         60                  65                  70

gga agc atg gtg tgg ctt ctc tca gct cct cct tat caa gag caa aaa   353
Gly Ser Met Val Trp Leu Leu Ser Ala Pro Pro Tyr Gln Glu Gln Lys
     75                  80                  85

agg gtg gct ctt ctg atg gca gct gca ctt ttt gaa ggc gcc tct att   401
Arg Val Ala Leu Leu Met Ala Ala Ala Leu Phe Glu Gly Ala Ser Ile
 90                  95                  100                 105

ggt cct ctg att gag ctg ggc att aac ttc gat cca agc att gtg ttt   449
Gly Pro Leu Ile Glu Leu Gly Ile Asn Phe Asp Pro Ser Ile Val Phe
                 110                 115                 120

ggc gct ttt gta ggt tgt gct gtg gtt ttt ggt tgc ttc tca gct gct   497
Gly Ala Phe Val Gly Cys Ala Val Val Phe Gly Cys Phe Ser Ala Ala
                 125                 130                 135

gcc atg ttg gca agg cgc agg gag tac ttg tac ctc ggg ggc ctt ctt   545
Ala Met Leu Ala Arg Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu
         140                 145                 150
```

```
tca tct ggc gtc tcc ctt ctc ttc tgg ttg cac ttt gca tcc tcc att    593
Ser Ser Gly Val Ser Leu Leu Phe Trp Leu His Phe Ala Ser Ser Ile
        155             160             165

ttt ggt ggt tcc atg gct gtt ttc aag ttt gag ttg tat ttt gga ctc    641
Phe Gly Gly Ser Met Ala Val Phe Lys Phe Glu Leu Tyr Phe Gly Leu
170             175             180             185

ttg gtg ttt gtg ggc tac atc gtc ttt gac acc caa gaa att att gag    689
Leu Val Phe Val Gly Tyr Ile Val Phe Asp Thr Gln Glu Ile Ile Glu
            190             195             200

aag gct cac ttg ggt gat atg gat tac gtt aag cat gca ttg acc ctt    737
Lys Ala His Leu Gly Asp Met Asp Tyr Val Lys His Ala Leu Thr Leu
        205             210             215

ttc aca gat ttt ggc gct gtt ttt gtg cgg att ctg atc atc atg tta    785
Phe Thr Asp Phe Gly Ala Val Phe Val Arg Ile Leu Ile Ile Met Leu
        220             225             230

aag aat gca tct gag aag gaa gag aag aag aag aag agg aga aac        830
Lys Asn Ala Ser Glu Lys Glu Glu Lys Lys Lys Lys Arg Arg Asn
        235             240             245

tagatttgct tctcaacttg tggtttccan aactccttgt gttcacctga aacaagcatg   890
ttaatagttt gatacttgct tcactttagc ataggctgtg atgtaatgtc gtgtgacatg   950
ccattatggc tgtgtgattg agcatctagc cttttatct tctaaagctt ttttcttaac   1010
attgataagg aaagttcctt gtga                                         1034

<210> 4
<211> 248
<212> PRT
<213> Lycopersicon esculentum

<400> 4
Met Glu Gly Phe Thr Ser Phe Phe Asp Ser Gln Ser Ala Ser Arg Asn
 1               5               10              15
Arg Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Leu
            20              25              30
Val Gln Thr His Leu Lys Gln Val Tyr Leu Thr Leu Cys Cys Ala Leu
        35              40              45
Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile Gly
    50              55              60
Gly Leu Leu Thr Thr Met Ala Cys Met Gly Ser Met Val Trp Leu Leu
65              70              75              80
Ser Ala Pro Pro Tyr Gln Glu Gln Lys Arg Val Ala Leu Leu Met Ala
            85              90              95
Ala Ala Leu Phe Glu Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu Gly
            100             105             110
Ile Asn Phe Asp Pro Ser Ile Val Phe Gly Ala Phe Val Gly Cys Ala
            115             120             125
Val Val Phe Gly Cys Phe Ser Ala Ala Ala Met Leu Ala Arg Arg Arg
    130             135             140
```

```
Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Val Ser Leu Leu
145             150             155             160
Phe Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Met Ala Val
            165             170             175
Phe Lys Phe Glu Leu Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Ile
            180             185             190
Val Phe Asp Thr Gln Glu Ile Ile Glu Lys Ala His Leu Gly Asp Met
            195             200             205
Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Phe Gly Ala Val
    210             215             220
Phe Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ala Ser Glu Lys Glu
225             230             235             240
Glu Lys Lys Lys Lys Arg Arg Asn
            245
```

<210> 5
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 5
ggaattcatg gaaggtttca catcgttc   28

<210> 6
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
ccgctcgagc tagggtcgac tgtttctcct cttcttcttc ttc   43

<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 7
ggaattcatg ccggaacatc ctgctgca   28